

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/774,192A
Source: 1FW16
Date Processed by STIC: 3/23/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/23/2007

PATENT APPLICATION: US/10/774,192A

TIME: 10:33:03

Input Set : A:\2872-US-CNT2 seq listing.txt

Output Set: N:\CRF4\03232007\J774192A.raw

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3 <110> APPLICANT: Sims, John
4      Born, Theresa
6 <120> TITLE OF INVENTION: ACPL DNA and Polypeptides
8 <130> FILE REFERENCE: 2872-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/774,192A
C--> 11 <141> CURRENT FILING DATE: 2004-02-06
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/01420
14 <151> PRIOR FILING DATE: 1999-01-22
16 <150> PRIOR APPLICATION NUMBER: 60/078,835
17 <151> PRIOR FILING DATE: 1998-03-20
19 <150> PRIOR APPLICATION NUMBER: 60/072,301
20 <151> PRIOR FILING DATE: 1998-01-23
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: PatentIn version 3.4
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1845
28 <212> TYPE: DNA
29 <213> ORGANISM: Mus sp.
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1845)
36 <400> SEQUENCE: 1
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38 Met Leu Cys Leu Gly Trp Val Phe Leu Trp Phe Val Ala Gly Glu Lys
39 1          5          10          15
41 acc aca gga ttt aat cat tca gct tgt gcc acc aaa aaa ctt ctg tgg      96
42 Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp
43          20          25          30
45 aca tat tct gca agg ggt gca gag aat ttt gtc cta ttt tgt gac tta      144
46 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu
47          35          40          45
49 caa gag ctt cag gag caa aaa ttc tcc cat gca agt caa ctg tca cca      192
50 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro
51 50          55          60
53 aca caa agt cct gct cac aaa cct tgc agt ggc agt cag aag gac cta      240
54 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu
55 65          70          75          80
57 tct gat gtc cag tgg tac atg caa cct cgg agt gga agt cca cta gag      288
58 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu
59          85          90          95
61 gag atc agt aga aac tct ccc cat atg cag agt gaa ggc atg ctg cat      336
62 Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His
63          100          105          110

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65	ata ttg gcc cca cag acg aac agc att tgg tca tat att tgt aga ccc	384
66	Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro	
67	115 120 125	
69	aga att agg agc ccc cag gat atg gcc tgt tgt atc aag aca gtc tta	432
70	Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu	
71	130 135 140	
73	gaa gtt aag cct cag aga aac gtg tcc tgt ggg aac aca gca caa gat	480
74	Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp	
75	145 150 155 160	
77	gaa caa gtc cta ctt ctt ggc agt act ggc tcc att cat tgt ccc agt	528
78	Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser	
79	165 170 175	
81	ctc agc tgc caa agt gat gta cag agt cca gag atg acc tgg tac aag	576
82	Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys	
83	180 185 190	
85	gat gga aga cta ctt cct gag cac aag aaa aat cca att gag atg gca	624
86	Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala	
87	195 200 205	
89	gat att tat ggt ggt aat caa ggc ttg tat gta tgt gat tac aca cag	672
90	Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln	
91	210 215 220	
93	tca gat aat gtg agt tcc tgg aca gtc cga gct gtg gtt aaa gtg aga	720
94	Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg	
95	225 230 235 240	
97	acc att ggt aag gac atc aat gtg aag ccg gaa att ctg gat ccc att	768
98	Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile	
99	245 250 255	
101	aca gat aca ctg gac gta gag ctt gga aag cct tta act ctc ccc tgc	816
102	Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys	
103	260 265 270	
105	aga gta cag ttt ggc ttc caa aga ctt tca aag cct gtg ata aag tgg	864
106	Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp	
107	275 280 285	
109	tat gtc aaa gaa tct aca cag gag tgg gaa atg tca gta ttt gag gag	912
110	Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu	
111	290 295 300	
113	aaa aga att caa tcc act ttc aag aat gaa gtc att gaa cgt acc atc	960
114	Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile	
115	305 310 315 320	
117	ttc ttg aga gaa gtt acc cag aga gat ctc agc aga aag ttt gtt tgc	1008
118	Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys	
119	325 330 335	
121	ttt gcc cag aac tcc att ggg aac aca aca cgg acc ata cgg ctg agg	1056
122	Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg	
123	340 345 350	
125	aag aag gaa gag gtg gtg ttt gta tac atc ctt ctc ggc acg gcc ttg	1104
126	Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu	
127	355 360 365	
129	atg ctg gtg ggc gtt ctg gtg gca gct gct ttc ctc tac tgg tac tgg	1152

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130 Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp
131      370      375      380
133 att gaa gtt gtc ctg ctc tgt cga acc tac aag aac aaa gat gag act      1200
134 Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr
135 385      390      395      400
137 ctg ggg gat aag aag gaa ttc gat gca ttt gta tcc tac tcg aat tgg      1248
138 Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp
139      405      410      415
141 agc tct cct gag act gac gcc gtg gga tct ctg agt gag gaa cac ctg      1296
142 Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu
143      420      425      430
145 gct ctg aat ctt ttc ccg gaa gtg cta gaa gac acc tat ggg tac aga      1344
146 Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg
147      435      440      445
149 ttg tgt ttg ctt gac cga gat gtg acc cca gga gga gtg tat gca gat      1392
150 Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp
151      450      455      460
153 gac att gtg agc atc att aag aaa agc cga aga gga ata ttt atc ctg      1440
154 Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu
155 465      470      475      480
157 agt ccc agc tac ctc aat gga ccc cgt gtc ttt gag cta caa gca gca      1488
158 Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala
159      485      490      495
161 gtg aat ctt gcc ttg gtt gat cag aca ctg aag ttg att tta att aag      1536
162 Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys
163      500      505      510
165 ttc tgt tcc ttc caa gag cca gaa tct ctt cct tac ctt gtc aaa aag      1584
166 Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys
167      515      520      525
169 gct ctg cgg gtt ctc ccc aca gtc aca tgg aaa ggc ttg aag tcg gtc      1632
170 Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val
171      530      535      540
173 cac gcc agt tcc agg ttc tgg acc caa att cgt tac cac atg cct gtg      1680
174 His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val
175 545      550      555      560
177 aag aac tcc aac agg ttt atg ttc aac ggg ctc aga att ttc ctg aag      1728
178 Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys
179      565      570      575
181 ggc ttt tcc cct gaa aag gac cta gtg aca cag aaa ccc ctg gaa gga      1776
182 Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly
183      580      585      590
185 atg ccc aag tct ggg aat gac cac gga gct cag aac ctc ctt ctc tac      1824
186 Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr
187      595      600      605
189 agt gac cag aag agg tgc tga      1845
190 Ser Asp Gln Lys Arg Cys
191      610
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 614

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196 <212> TYPE: PRT
197 <213> ORGANISM: Mus sp.
199 <400> SEQUENCE: 2
201 Met Leu Cys Leu Gly Trp Val Phe Leu Trp Phe Val Ala Gly Glu Lys
202 1 5 10 15
205 Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp
206 20 25 30
209 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu
210 35 40 45
213 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro
214 50 55 60
217 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu
218 65 70 75 80
221 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu
222 85 90 95
225 Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His
226 100 105 110
229 Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro
230 115 120 125
233 Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu
234 130 135 140
237 Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp
238 145 150 155 160
241 Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser
242 165 170 175
245 Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys
246 180 185 190
249 Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala
250 195 200 205
253 Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln
254 210 215 220
257 Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg
258 225 230 235 240
261 Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile
262 245 250 255
265 Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys
266 260 265 270
269 Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp
270 275 280 285
273 Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu
274 290 295 300
277 Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile
278 305 310 315 320
281 Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys
282 325 330 335
285 Phe Ala Gln Asn Ser Ile Gly Asn Thr Arg Thr Ile Arg Leu Arg
286 340 345 350
289 Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu
290 355 360 365

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Input Set : A:\2872-US-CNT2 seq listing.txt

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293 Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp
294      370                      375                      380
297 Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr
298 385                      390                      395                      400
301 Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp
302                      405                      410                      415
305 Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu
306                      420                      425                      430
309 Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg
310                      435                      440                      445
313 Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp
314 450                      455                      460
317 Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu
318 465                      470                      475                      480
321 Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala
322                      485                      490                      495
325 Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys
326                      500                      505                      510
329 Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys
330                      515                      520                      525
333 Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val
334 530                      535                      540
337 His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val
338 545                      550                      555                      560
341 Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys
342                      565                      570                      575
345 Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly
346                      580                      585                      590
349 Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr
350 595                      600                      605
353 Ser Asp Gln Lys Arg Cys
354 610
357 <210> SEQ ID NO: 3
358 <211> LENGTH: 754
359 <212> TYPE: DNA
360 <213> ORGANISM: Homo sapiens
363 <220> FEATURE:
364 <221> NAME/KEY: misc_feature
365 <222> LOCATION: (6)..(8)
366 <223> OTHER INFORMATION: "n" = a, t, c, g
368 <220> FEATURE:
369 <221> NAME/KEY: misc_feature
370 <222> LOCATION: (563)..(563)
371 <223> OTHER INFORMATION: "n" = a, t, c, g
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (596)..(596)
376 <223> OTHER INFORMATION: "n" = a, t, c, g
378 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/23/2007
PATENT APPLICATION: US/10/774,192A TIME: 10:33:04

Input Set : A:\2872-US-CNT2 seq listing.txt
Output Set: N:\CRF4\03232007\J774192A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. ~~6,7,8,563,596,607,708,729,752~~

VERIFICATION SUMMARY

DATE: 03/23/2007

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TIME: 10:33:04

Input Set : A:\2872-US-CNT2 seq listing.txt

Output Set: N:\CRF4\03232007\J774192A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:540
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:600
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:660
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:720